

SEQUENCE LISTING

<110> Dhugga, Kanwarpal S.
 Niu, Xiaomu
 Helentjaris, Timothy

<120> Manipulation of Sucrose Synthase Genes
 to Improve Stalk and Grain Quality

<130> 1301

<150> 60/270,777
 <151> 2001-02-22

<160> 13

<170> FastSEQ for Windows Version 4.0

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 <213> Zea mays

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gatgcatgaa	ctcatcaaga	cccacaactt	gttcgggca	ttccgcttga	tctctgccc	1920

1000014-000002

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gcttcctact	ttcgcgacgc	tccatggagg	tccagctgag	atcatagagc	atggcgcttc	2100
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 Gly Ile Leu Gln Pro His His Ile Leu Asp Ala Leu Asp Glu Val Gln
 35 40 45
 Gly Ser Gly Gly Arg Ala Leu Ala Glu Gly Pro Phe Leu Asp Val Leu
 50 55 60
 Arg Ser Ala Gln Glu Ala Ile Val Leu Pro Pro Phe Val Ala Ile Ala
 65 70 75 80
 Val Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val His
 85 90 95
 Glu Leu Ser Val Glu Gln Leu Thr Val Ser Glu Tyr Leu Arg Phe Lys
 100 105 110
 Glu Glu Leu Val Asp Gly Gln His Asn Asp Pro Tyr Val Leu Glu Leu
 115 120 125
 Asp Phe Glu Pro Phe Asn Val Ser Val Pro Arg Pro Asn Arg Ser Ser
 130 135 140
 Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Ile
 145 150 155 160
 Met Phe Arg Asn Arg Asp Cys Leu Glu Pro Leu Leu Asp Phe Leu Arg
 165 170 175
 Gly His Arg His Lys Gly His Val Met Met Leu Asn Asp Arg Ile Gln
 180 185 190
 Ser Leu Gly Arg Leu Gln Ser Val Leu Thr Lys Ala Glu Glu His Leu
 195 200 205
 Ser Lys Leu Pro Ala Asp Thr Pro Tyr Ser Gln Phe Ala Tyr Lys Phe
 210 215 220
 Gln Glu Trp Gly Leu Glu Lys Gly Trp Gly Asp Thr Ala Gly His Val
 225 230 235 240
 Leu Glu Met Ile His Leu Leu Leu Asp Ile Ile Gln Ala Pro Asp Pro
 245 250 255
 Ser Thr Leu Glu Lys Phe Leu Gly Arg Ile Pro Met Ile Phe Asn Val
 260 265 270
 Val Val Val Ser Pro His Gly Tyr Phe Gly Gln Ala Asn Val Leu Gly
 275 280 285
 Leu Pro Asp Thr Gly Gly Gln Ile Val Tyr Ile Leu Asp Gln Val Arg

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290	295	300
Ala Leu Glu Asn Glu Met Val Leu Arg Leu Lys Lys Gln Gly Leu Asp		
305	310	315
Val Ser Pro Lys Ile Leu Ile Val Thr Arg Leu Ile Pro Asp Ala Lys		320
325	330	335
Gly Thr Ser Cys Asn Gln Arg Leu Glu Arg Ile Ser Gly Thr Gln His		
340	345	350
Thr Tyr Ile Leu Arg Val Pro Phe Arg Asn Glu Asn Gly Ile Leu Lys		
355	360	365
Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu Glu Thr Phe Ala		
370	375	380
Glu Asp Ala Ala Gly Glu Ile Ala Ala Glu Leu Gln Gly Thr Pro Asp		
385	390	395
Phe Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu		400
405	410	415
Ser Tyr Lys Met Gly Ile Thr Gln Cys Asn Ile Ala His Ala Leu Glu		
420	425	430
Lys Thr Lys Tyr Pro Asp Ser Asp Ile Phe Trp Lys Asn Phe Asp Glu		
435	440	445
Lys Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Ile Ile Ala Met Asn		
450	455	460
Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser		
465	470	475
Lys Asn Thr Val Gly Gln Tyr Glu Ser His Thr Ala Phe Thr Leu Pro		
485	490	495
Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe		
500	505	510
Asn Ile Val Ser Pro Gly Ala Asp Met Ser Ile Tyr Phe Pro His Thr		
515	520	525
Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu		
530	535	540
Ile Tyr Asp Pro Glu Gln Asn Asp Glu His Ile Gly His Leu Asp Asp		
545	550	555
Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg Val Lys		
565	570	575
Asn Ile Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg		
580	585	590
Glu Leu Val Asn Leu Val Val Ala Gly Tyr Asn Asp Val Asn Lys		
595	600	605
Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu		
610	615	620
Ile Lys Thr His Asn Leu Phe Gly Gln Phe Arg Trp Ile Ser Ala Gln		
625	630	635
Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr		
645	650	655
His Gly Ala Phe Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr		
660	665	670
Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His		
675	680	685
Gly Gly Pro Ala Glu Ile Ile Glu His Gly Val Ser Gly Phe His Ile		
690	695	700
Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe Phe		
705	710	715
Asp Arg Cys Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala		
725	730	735
Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile Tyr Ser Glu		
740	745	750
Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser		

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755	760	765
Lys Leu Glu Arg Leu Glu	Thr Arg Arg Tyr Leu Glu	Met Phe Tyr Ile
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Pro Gln		800

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 <211> 36
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 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon the adapter
 sequence and poly T to remove clones which have a
 poly A tail but no cDNA.

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 <213> Zea mays

<220>
 <221> CDS
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 accatcgagc c atg gct gcc aag ctg act cgc ctt cac agt ctt cgc gaa 110
 Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu
 1 5 10

cgc ctt ggt gcc acc ttc tcc tcc cat ccc aat gaa ctg ata gca ctc 158
 Arg Leu Gly Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu
 15 20 25

ttt tcc agg tat gtt cac cag ggc aag gga atg ctt cag cgc cat cag 206
 Phe Ser Arg Tyr Val His Gln Gly Lys Met Leu Gln Arg His Gln
 30 35 40 45

ctg ctt gcg gag ttt gat gcc ctg ttt gat agt gac aag gag aag tat 254
 Leu Leu Ala Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr
 50 55 60

gca cca ttt gaa gac att ctt cgt gct gtc cag gaa gca att gtg ctc 302
 Ala Pro Phe Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu
 65 70 75

ccc cca tgg gtt gca ctt gct atc agg cca agg cct ggt gtc tgg gat 350
 Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp
 80 85 90

tac att cgg gtg aat gta agt gag ctg gct gtg gag gag ctg agt gtt 398

1000011111000000

Tyr Ile Arg Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val			
95	100	105	
tct gag tac ttg gca ttc aag gaa cag ctg gtg gat gga caa tcc aac			446
Ser Glu Tyr Leu Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn			
110	115	120	125
agc aac ttt gtg ctt gag ctt gat ttt gag ccc ttc aat gcc tcc ttt			494
Ser Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe			
130	135	140	
cct cgt cct tcc atg tcg aag tcc atc gga aat gga gtg caa ttc ctt			542
Pro Arg Pro Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu			
145	150	155	
aac cga cac ctg tcg tcc aag ttg ttc cag gac aag gag agt ttg tac			590
Asn Arg His Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr			
160	165	170	
ccc ttg ctg aac ttc ctc aag gct cat aac tac aag ggc acg acg atg			638
Pro Leu Leu Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met			
175	180	185	
atg ttg aat gac aga atc caa agc ctt cgt ggt ctc caa tca tcc ctg			686
Met Leu Asn Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ser Leu			
190	195	200	205
aga aag gca gag gag tat cta ctg agt gtt cct caa gac act ccc tac			734
Arg Lys Ala Glu Glu Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr			
210	215	220	
tcg gag ttc aac cat agg ttc caa gag ctt ggc ttg gag aag ggt tgg			782
Ser Glu Phe Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp			
225	230	235	
ggt gac act gcg aag cgt gtt ctc gac aca ctc cac ttg ctt ctc gac			830
Gly Asp Thr Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp			
240	245	250	
ctt ctt gag gcc cct gat cct gcc aac ttg gag aag ttc ctt gga act			878
Leu Leu Glu Ala Pro Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr			
255	260	265	
ata cca atg atg ttc aac gtt gtt atc ctg tct cct cat ggc tac ttc			926
Ile Pro Met Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe			
270	275	280	285
gcc cag tcc aat gtg ctt gga tac cct gac act ggc ggt cag gtt gtg			974
Ala Gln Ser Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val			
290	295	300	
tac att ctg gat caa gtc cgt gct ttg gag aat gag atg ctt ctg agg			1022
Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg			
305	310	315	
att aag cag caa ggc ctt gat atc act ccg aag atc ctc att gtt acc			1070
Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr			
320	325	330	

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agg ctg ttg cct gat gct gct ggg act acg tgc ggt cag cgg ctg gag	335	340	345	1118
Arg Leu Leu Pro Asp Ala Ala Gly Thr Thr Cys Gly Gln Arg Leu Glu				
aag gtc att ggt act gag cac aca gac atc att cgc gtt ccc ttc aga	350	355	360	1166
Lys Val Ile Gly Thr Glu His Thr Asp Ile Ile Arg Val Pro Phe Arg				
aat gag aat ggc atc ctc cgc aag tgg atc tct cgt ttt gat gtc tgg	370	375	380	1214
Asn Glu Asn Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp				
cca tac ctg gag aca tac act gag gat gtt tcc agt gaa ata atg aaa	385	390	395	1262
Pro Tyr Leu Glu Thr Tyr Glu Asp Val Ser Ser Glu Ile Met Lys				
gaa atg cag gcc aag cct gac ctt atc att ggc aac tac agc gat ggc	400	405	410	1310
Glu Met Gln Ala Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly				
aac cta gtc gcc act ctg ctc gcg cac aag ttg gga gtc act cag tgt	415	420	425	1358
Asn Leu Val Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys				
acc atc gct cat gcc ttg gag aaa acc aaa tac ccc aac tcg gac atc	430	435	440	1406
Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile				
tac ttg gac aaa ttc gac agc cag tac cac ttc tct tgc cag ttc aca	450	455	460	1454
Tyr Leu Asp Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr				
gct gac ctt att gcc atg aac cac acc gat ttc atc atc acc agc aca	465	470	475	1502
Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr				
ttc caa gaa atc gcg gga agc aag gac acc gtc gag ggg cag tac gag tcc	480	485	490	1550
Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser				
cat atc gcg ttc act ctt cct ggg ctc tac cgt gtc cat ggc atc	495	500	505	1598
His Ile Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile				
gat gtt ttc gat ccc aag ttc aac att gtc tct cct gga gca gac atg	510	515	520	1646
Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met				
agt gtt tac tac cct tat acg gaa acc gac aag aga ctc act gcc ttc	530	535	540	1694
Ser Val Tyr Tyr Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe				
cat cct gaa atc gag gag ctc atc tac agc gac gtc gag aac tcc gag	545	550	555	1742
His Pro Glu Ile Glu Glu Leu Ile Tyr Ser Asp Val Glu Asn Ser Glu				
cac aag ttc gtg ctg aag gac aag aag aag ccg atc atc ttc tcg atg				1790

2022年3月

His Lys Phe Val Leu Lys Asp Lys Lys Pro Ile Ile Phe Ser Met	560	565	570	
gct cgt ctc gac cgc gtg aag aac atg aca ggc ctg gtc gag atg tac	575	580	585	1838
Ala Arg Leu Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Tyr				
gct aag aac gct cgc ctg agg gag ctg gct aac ctc gtg atc gtt gcc	590	595	600	1886
Gly Lys Asn Ala Arg Leu Arg Glu Leu Ala Asn Leu Val Ile Val Ala				
ggt gac cac ggc aag gag tcc aag gac agg gag gag cag gct gag ttc	610	615	620	1934
Gly Asp His Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe				
aag aag atg tac agc ctc atc gac gag tac aag ttg aag ggc cat atc	625	630	635	1982
Lys Lys Met Tyr Ser Leu Ile Asp Glu Tyr Lys Leu Lys Gly His Ile				
cggtggatc tcg gct cag atg aac cgt gtc cgc aac ggg gag ctg tac	640	645	650	2030
Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr				
cgc tac att tgc gat acc aag ggc gca ttc gtg cag cct gct ttc tac	655	660	665	2078
Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr				
gaa gct ttc ggc ctg act gtg atc gag tcc atg acg tgc ggt ctg cca	670	675	680	2126
Glu Ala Phe Gly Leu Thr Val Ile Glu Ser Met Thr Cys Gly Leu Pro				
acg atc gct acc tgc cat ggc ggc cct gct gag atc atc gtg gac ggg	690	695	700	2174
Thr Ile Ala Thr Cys His Gly Pro Ala Glu Ile Ile Val Asp Gly				
gta tct ggc ctg cac att gac cct tac cac agc gac aag gcc gct gat	705	710	715	2222
Val Ser Gly Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp				
atc ctg gtc aac ttc ttt gac aaa tgc aag gca gat ccc agc tac tgg	720	725	730	2270
Ile Leu Val Asn Phe Asp Lys Cys Lys Ala Asp Pro Ser Tyr Trp				
gac gag atc tca cag ggc ggc ctg cag aga att tat gag aag tac acc	735	740	745	2318
Asp Glu Ile Ser Gln Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr				
tgg aag ctc tac tcc gag agg ctg atg acc ctg acc ggc gtg tac ggg	750	755	760	2366
Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly				
ttc tgg aag tac gtg agc aac ctg gag agg cgc gag acc cgc cgc tac	770	775	780	2414
Phe Trp Lys Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr				
atc gag atg ttc tac gcc ctg aag tac cgt agc ctg gca agc cag gtt	785	790	795	2462
Ile Glu Met Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ser Gln Val				

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Pro Leu Ser Phe Asp *	
800	
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agtgcgtgtat tggagttatg tgtacttggt ttccaagaac tttggttcct tctcgtttt	2630
tttcctgtt tgagcgtttt tggcagcgc tggcctggc cctagatgg tgggaattgg	2690
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Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Ala	
35 40 45	
Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr Ala Pro Phe	
50 55 60	
Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp	
65 70 75 80	
Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg	
85 90 95	
Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val Ser Glu Tyr	
100 105 110	
Leu Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn Ser Asn Phe	
115 120 125	
Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro	
130 135 140	
Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His	
145 150 155 160	
Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu	
165 170 175	
Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met Met Leu Asn	
180 185 190	
Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ser Leu Arg Lys Ala	
195 200 205	
Glu Glu Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr Ser Glu Phe	
210 215 220	
Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr	
225 230 235 240	
Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp Leu Leu Glu	
245 250 255	
Ala Pro Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr Ile Pro Met	
260 265 270	
Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser	
275 280 285	
Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu	
290 295 300	
Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln	
305 310 315 320	
Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu	
325 330 335	

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Pro Asp Ala Ala Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Ile
340 345 350
Gly Thr Glu His Thr Asp Ile Ile Arg Val Pro Phe Arg Asn Glu Asn
355 360 365
Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu
370 375 380
Glu Thr Tyr Thr Glu Asp Val Ser Ser Glu Ile Met Lys Glu Met Gln
385 390 395 400
Ala Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val
405 410 415
Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys Thr Ile Ala
420 425 430
His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp
435 440 445
Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Leu
450 455 460
Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu
465 470 475 480
Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser His Ile Ala
485 490 495
Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
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Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met Ser Val Tyr
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Tyr Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
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Ile Glu Glu Leu Ile Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe
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Val Leu Lys Asp Lys Lys Pro Ile Ile Phe Ser Met Ala Arg Leu
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Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Tyr Gly Lys Asn
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Ala Arg Leu Arg Glu Leu Ala Asn Leu Val Ile Val Ala Gly Asp His
595 600 605
Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Lys Met
610 615 620
Tyr Ser Leu Ile Asp Glu Tyr Lys Leu Lys Gly His Ile Arg Trp Ile
625 630 635 640
Ser Ala Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr Arg Tyr Ile
645 650 655
Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
660 665 670
Gly Leu Thr Val Ile Glu Ser Met Thr Cys Gly Leu Pro Thr Ile Ala
675 680 685
Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asp Gly Val Ser Gly
690 695 700
Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
705 710 715 720
Asn Phe Phe Asp Lys Cys Lys Ala Asp Pro Ser Tyr Trp Asp Glu Ile
725 730 735
Ser Gln Gly Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
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Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
755 760 765
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Leu Ser Arg Leu His Ser Val Arg Glu Arg Ile Gly Asp Ser Leu Ser
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Ala His Pro Asn Glu Leu Val Ala Val Phe Thr Arg Leu Lys Asn Leu
30 35 40

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Gly Lys Gly Met Leu Gln Pro His Gln Ile Ile Ala Glu Tyr Asn Asn
45 50 55

gcg atc cct gag gct gag cgc gag aag ctc aag gat ggt gct ttt gag 246
Ala Ile Pro Glu Ala Glu Arg Glu Lys Leu Lys Asp Gly Ala Phe Glu
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gat gtc ctg agg gca gct cag gag gcg att gtc atc ccc cca tgg gtt 294
Asp Val Leu Arg Ala Ala Gln Glu Ala Ile Val Ile Pro Pro Trp Val
75 80 85

gca ctt gcc atc cgc cct agg cct ggt gtc tgg gag tat gtg agg gtc 342
Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Val
90 95 100 105

aac gtc agt gag ctc gct gtt gag gag ctg aga gtt cct gag tac ctg 390
Asn Val Ser Glu Leu Ala Val Glu Glu Leu Arg Val Pro Glu Tyr Leu
110 115 120

cag ttc aag gaa cag ctt gtg gaa gaa ggc ccc aac aac aac ttt gtt 438
Gln Phe Lys Glu Gln Leu Val Glu Glu Gly Pro Asn Asn Phe Val
125 130 135

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Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro Ser
140 145 150

ctg tca aag tcc att ggc aat ggc gtg cag ttc ctc aac agg cac ctg 534
Leu Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu
155 160 165

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tca tca aag ctc ttc cat gac aag gag agc atg tac ccc ttg ctc aac	582
Ser Ser Lys Leu Phe His Asp Lys Glu Ser Met Tyr Pro Leu Leu Asn	
170 175 180 185	
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Phe Leu Arg Ala His Asn Tyr Lys Gly Met Thr Met Met Leu Asn Asp	
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Arg Ile Arg Ser Leu Ser Ala Leu Gln Gly Ala Leu Arg Lys Ala Glu	
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gag cac ctg tcc acc cta caa gct gat acc cca tac tct gaa ttt cac	726
Glu His Leu Ser Thr Leu Gln Ala Asp Thr Pro Tyr Ser Glu Phe His	
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cac agg ttc cag gaa ctt ggt ctg gag aag ggt tgg ggt gat tgc gct	774
His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Cys Ala	
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Lys Arg Ala Gln Glu Thr Ile His Leu Leu Leu Asp Leu Leu Glu Ala	
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Pro Asp Pro Ser Thr Leu Glu Lys Phe Leu Gly Thr Ile Pro Met Val	
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Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ala Asn	
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gtc ttg ggt tac cct gac acc gga ggc cag gtt gtc tac atc ttg gat	966
Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu Asp	
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Gln Val Arg Ala Met Glu Asn Glu Met Leu Leu Arg Ile Lys Gln Cys	
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Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu Pro	
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Thr Glu His Cys His Ile Leu Arg Val Pro Phe Arg Thr Glu Asn Gly	
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Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Val Trp Pro Tyr Leu Glu	
380 385 390	
act tac act gat gac gtg gcg cat gag att gct gga gag ctt cag gcc	1254
Thr Tyr Thr Asp Asp Val Ala His Glu Ile Ala Gly Glu Leu Gln Ala	

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aat cct gac ctg atc atc gga aac tac agt gac gga aac ctt gtt gcg Asn Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala 410 415 420 425			1302
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ttt gag gat cac tac cac ttc tcg tgc cag ttc acc act gac ttg att Phe Glu Asp His Tyr His Phe Ser Cys Gln Phe Thr Thr Asp Leu Ile 460 465 470			1446
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ccc aag ttc aac atc gtg tct cct ggc gcg gac ctg tcc atc tac ttc Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Leu Ser Ile Tyr Phe 525 530 535			1638
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810 815	
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<213> Zea mays

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35 40 45
His Gln Ile Ile Ala Glu Tyr Asn Asn Ala Ile Pro Glu Ala Glu Arg
50 55 60
Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala Gln
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Glu Ala Ile Val Ile Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
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Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Ala Val
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Glu Glu Leu Arg Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
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Glu Glu Gly Pro Asn Asn Asn Phe Val Leu Glu Leu Asp Phe Glu Pro
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Phe Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn
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Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp
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Lys Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr
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Lys Gly Met Thr Met Met Leu Asn Asp Arg Ile Arg Ser Leu Ser Ala
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Leu Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Thr Leu Gln
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Ala Asp Thr Pro Tyr Ser Glu Phe His His Arg Phe Gln Glu Leu Gly
225 230 235 240
Leu Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu Thr Ile
245 250 255
His Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu
260 265 270
Lys Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser
275 280 285
Pro His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr
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Gly Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn
305 310 315 320
Glu Met Leu Leu Arg Ile Lys Gln Cys Gly Leu Asp Ile Thr Pro Lys
325 330 335
Ile Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Thr Gly Thr Thr Cys
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Gly Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Cys His Ile Leu
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Arg Val Pro Phe Arg Thr Glu Asn Gly Ile Val Arg Lys Trp Ile Ser
370 375 380
Arg Phe Glu Val Trp Pro Tyr Leu Glu Thr Tyr Thr Asp Asp Val Ala
385 390 395 400
His Glu Ile Ala Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly
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Asn Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Met
420 425 430

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Pro Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe
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465 470 475 480
Ile Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val
485 490 495
Gly Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg
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Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser
515 520 525
Pro Gly Ala Asp Leu Ser Ile Tyr Phe Pro Tyr Thr Glu Ser His Lys
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Arg Leu Thr Ser Leu His Pro Glu Ile Glu Glu Leu Leu Tyr Ser Gln
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Thr Glu Asn Thr Glu His Lys Phe Val Leu Asn Asp Arg Asn Lys Pro
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Ile Ile Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly
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Leu Val Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu
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Glu Gln Ala Glu Phe Lys Lys Met Phe Asp Leu Ile Glu Gln Tyr Asn
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690 695 700
Ile Ile Val His Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Gly
705 710 715 720
Asp Lys Ala Ser Ala Leu Leu Val Asp Phe Phe Asp Lys Cys Gln Ala
725 730 735
Glu Pro Ser His Trp Ser Lys Ile Ser Gln Gly Gly Leu Gln Arg Ile
740 745 750
Glu Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu
755 760 765
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DO NOT EDIT - ORIGIN

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gag gac acc ctc cac gcg cac cgc aac gag ctc gtc gcc ctc ctc tcc 96
Glu Asp Thr Leu His Ala His Arg Asn Glu Leu Val Ala Leu Leu Ser
20 25 30

aag tac gtg aac aag ggg aag ggc atc ctg cag cgc cac cac atc ctc 144
Lys Tyr Val Asn Lys Gly Lys Ile Leu Gln Pro His His Ile Leu
35 40 45

gac gcg ctc gac gag gtc cag ggc tcc ggg gtc cgc gcg ctc gcc gag 192
Asp Ala Leu Asp Glu Val Gln Gly Ser Gly Val Arg Ala Leu Ala Glu
50 55 60

gga ccc ttc ctc gac gtc ctc cgc tcc gcg cag gag gcg atc gtg ctg 240
Gly Pro Phe Leu Asp Val Leu Arg Ser Ala Gln Glu Ala Ile Val Leu
65 70 75 80

ccg ccg ttc gtg gcc atc gcg gtg cgc cgc ccg gga gtt tgg gag 288
Pro Pro Phe Val Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu

MOBILITY - DRAFT

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gat ccc tac gtt ctc gag ctt gac ttc gag ccg ttc aat gtc tca gtc Asp Pro Tyr Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Val Ser Val 130 135 140			480
cca cgc cca aat cgg tca tca tct att gga aac ggt gtg cag ttc ctc Pro Arg Pro Asn Arg Ser Ser Ile Gly Asn Gly Val Gln Phe Leu 145 150 155 160			528
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ccc ctg ttg gat ttc ctc cgt ggc cac cgg cac aag ggg cat gtt atg Pro Leu Leu Asp Phe Leu Arg Gly His Arg His Lys Gly His Val Met 180 185 190			624
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cca tat ctg gaa aca ttt gct gag gat gct gct ggt gaa att gct gct Pro Tyr Leu Glu Thr Phe Ala Glu Asp Ala Ala Gly Glu Ile Ala Ala 385	390	395	1200
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aat ctt gtg gcg tca ttg cta tct tac aag atg gga att acc cag tgc Asn Leu Val Ala Ser Leu Leu Ser Tyr Lys Met Gly Ile Thr Gln Cys 420	425	430	1296
aac att gct cat gct ctg gaa aag act aag tat cca gat tca gac ata Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile 435	440	445	1344
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gat gtc ttc gat cca aag ttc aat ata gtc tct cct gga gct gac atg Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met 515	520	525	1584
tcc ata tac ttt cca cat acc gag aag gcc aag cga ctc acc tct ctt Ser Ile Tyr Phe Pro His Thr Glu Lys Ala Lys Arg Leu Thr Ser Leu 530	535	540	1632
cat ggt tca atc gaa aat ttg att tat gac ccg gag caa aac gat gaa His Gly Ser Ile Glu Asn Leu Ile Tyr Asp Pro Glu Gln Asn Asp Glu 550	555	560	1680

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gct aag tgc gct aag ctg agg gag ctg gta aac ctt gtc gtc gtt gcc Ala Lys Cys Ala Lys Leu Arg Glu Leu Val Asn Leu Val Val Val Ala 595 600 605 1824					
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tat cgc tac atc gct gat acc cat ggt gct ttc gta cag ccg gcc ttg Tyr Arg Tyr Ile Ala Asp Thr His Gly Ala Phe Val Gln Pro Ala Leu 660 665 670 2016					
tat gaa gcg ttc ggt ctc acc gtc gtt gag gcc atg acc tgg tgg ctt Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu 675 680 685 2064					
cct act ttc gcg acg ctc cat gga ggt cca gct gag atc ata gag cat Pro Thr Phe Ala Thr Leu His Gly Gly Pro Ala Glu Ile Ile Glu His 690 695 700 2112					
ggc gtc tcg ggc ttc cac att gac ccg tac cac ccc gaa cag gct gtt Gly Val Ser Gly Phe His Ile Asp Pro Tyr His Pro Glu Gln Ala Val 705 710 715 720 2160					
aat ctg atg gcc gac ttc ttc gac ccg tgc aag caa gac cca gat cac Asn Leu Met Ala Asp Phe Phe Asp Arg Cys Lys Gln Asp Pro Asp His 725 730 735 2208					
tgg gtg aat ata tct gga gca ggg ctg cag cgc ata tac gag aag tac Trp Val Asn Ile Ser Gly Ala Gly Leu Gln Arg Ile Tyr Glu Lys Tyr 740 745 750 2256					
aca tgg aag ata tac tca gag agg ttg atg aca ctg gcc ggg gtc tac Thr Trp Lys Ile Tyr Ser Glu Arg Leu Met Thr Leu Ala Gly Val Tyr 755 760 765 2304					
gg ^t ttc tgg aag tac gtg tcg aag ctc gag agg ctg gag acg agg cgc Gly Phe Trp Lys Tyr Val Ser Lys Leu Glu Arg Leu Glu Thr Arg Arg 770 775 780 2352					

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Tyr Leu Glu Met Phe Tyr Ile Leu Lys Phe Arg Glu Leu Ala Lys Thr
785 790 795 800

gtg ccg ctt gca att gac caa ccg cag tag cttgcgcaac tgcgactg 2450
Val Pro Leu Ala Ile Asp Gln Pro Gln *
8.05

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35 40 45
Asp Ala Leu Asp Glu Val Gln Gly Ser Gly Val Arg Ala Leu Ala Glu
50 55 60
Gly Pro Phe Leu Asp Val Leu Arg Ser Ala Gln Glu Ala Ile Val Leu
65 70 75 80
Pro Pro Phe Val Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu
85 90 95
Tyr Val Arg Val Asn Val His Glu Leu Ser Val Glu Gln Leu Thr Val
100 105 110
Ser Glu Tyr Leu Arg Phe Lys Glu Glu Leu Val Asp Gly Gln His Asn
115 120 125
Asp Pro Tyr Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Val Ser Val
130 135 140
Pro Arg Pro Asn Arg Ser Ser Ser Ile Gly Asn Gly Val Gln Phe Leu
145 150 155 160
Asn Arg His Leu Ser Ser Ile Met Phe Arg Asn Arg Asp Cys Leu Glu
165 170 175
Pro Leu Leu Asp Phe Leu Arg Gly His Arg His Lys Gly His Val Met
180 185 190
Met Leu Asn Asp Arg Ile Gln Ser Leu Gly Arg Leu Gln Ser Val Leu
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Thr Lys Ala Glu Glu His Leu Ser Lys Leu Pro Ala Asp Thr Pro Tyr
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Ser Gln Phe Ala Tyr Lys Phe Gln Glu Trp Gly Leu Glu Lys Gly Trp
225 230 235 240
Gly Asp Thr Ala Gly His Val Leu Glu Met Ile His Leu Leu Leu Asp
245 250 255
Ile Ile Gln Ala Pro Asp Pro Ser Thr Leu Glu Lys Phe Leu Gly Arg
260 265 270

Ile Pro Met Ile Phe Asn Val Val Val Val Ser Pro His Gly Tyr Phe
275 280 285
Gly Gln Ala Asn Val Leu Gly Leu Pro Asp Thr Gly Gly Gln Ile Val
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Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Val Leu Arg
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Leu Lys Lys Gln Gly Leu Asp Val Ser Pro Lys Ile Leu Ile Val Thr
325 330 335
Arg Leu Ile Pro Asp Ala Lys Gly Thr Ser Cys Asn Gln Arg Leu Glu
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Arg Ile Ser Gly Thr Gln His Thr Tyr Ile Leu Arg Val Pro Phe Arg
355 360 365
Asn Glu Asn Gly Ile Leu Lys Lys Trp Ile Ser Arg Phe Asp Val Trp
370 375 380
Pro Tyr Leu Glu Thr Phe Ala Glu Asp Ala Ala Gly Glu Ile Ala Ala
385 390 395 400
Glu Leu Gln Gly Thr Pro Asp Phe Ile Ile Gly Asn Tyr Ser Asp Gly
405 410 415
Asn Leu Val Ala Ser Leu Leu Ser Tyr Lys Met Gly Ile Thr Gln Cys
420 425 430
Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile
435 440 445
Phe Trp Lys Asn Phe Asp Glu Lys Tyr His Phe Ser Cys Gln Phe Thr
450 455 460
Ala Asp Ile Ile Ala Met Asn Asn Ala Asp Phe Ile Ile Thr Ser Thr
465 470 475 480
Tyr Gln Glu Ile Ala Gly Ser Lys Asn Thr Val Gly Gln Tyr Glu Ser
485 490 495
His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile
500 505 510
Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met
515 520 525
Ser Ile Tyr Phe Pro His Thr Glu Lys Ala Lys Arg Leu Thr Ser Leu
530 535 540
His Gly Ser Ile Glu Asn Leu Ile Tyr Asp Pro Glu Gln Asn Asp Glu
545 550 555 560
His Ile Gly His Leu Asp Asp Arg Ser Lys Pro Ile Leu Phe Ser Met
565 570 575
Ala Arg Leu Asp Arg Val Lys Asn Ile Thr Gly Leu Val Glu Ala Phe
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Ala Lys Cys Ala Lys Leu Arg Glu Leu Val Asn Leu Val Val Val Ala
595 600 605
Gly Tyr Asn Asp Val Asn Lys Ser Lys Asp Arg Glu Glu Ile Ala Glu
610 615 620
Ile Glu Lys Met His Glu Leu Ile Lys Thr His Asn Leu Phe Gly Gln
625 630 635 640
Phe Arg Trp Ile Ser Ala Gln Thr Asn Arg Ala Arg Asn Gly Glu Leu
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Tyr Arg Tyr Ile Ala Asp Thr His Gly Ala Phe Val Gln Pro Ala Leu
660 665 670
Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu
675 680 685
Pro Thr Phe Ala Thr Leu His Gly Gly Pro Ala Glu Ile Ile Glu His
690 695 700
Gly Val Ser Gly Phe His Ile Asp Pro Tyr His Pro Glu Gln Ala Val
705 710 715 720
Asn Leu Met Ala Asp Phe Phe Asp Arg Cys Lys Gln Asp Pro Asp His
725 730 735

Trp Val Asn Ile Ser Gly Ala Gly Leu Gln Arg Ile Tyr Glu Lys Tyr
740 745 750
Thr Trp Lys Ile Tyr Ser Glu Arg Leu Met Thr Leu Ala Gly Val Tyr
755 760 765
Gly Phe Trp Lys Tyr Val Ser Lys Leu Glu Arg Leu Glu Thr Arg Arg
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